

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/574,819

DATE: 07/31/2001
TIME: 14:00:36

Input Set : N:\Crf3\RULE60\09574819.txt
Output Set: N:\CRF3\07312001\I574819.raw

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: Luyten, Frank P.
8 Moos, Jr., Malcolm
9 Chang, Steven Chao-Huan
11 (ii) TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
12 PROTEINS

14 (iii) NUMBER OF SEQUENCES: 24

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Knobbe, Martens, Olson & Bear
18 (B) STREET: 620 Newport Center Drive, 16th Floor
19 (C) CITY: Newport Beach
20 (D) STATE: CA
21 (E) COUNTRY: U.S.A.
22 (F) ZIP: 92660

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Diskette
26 (B) COMPUTER: IBM Compatible
27 (C) OPERATING SYSTEM: Windows
28 (D) SOFTWARE: FastSEQ for Windows Version 2.0b

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/574,819

C--> 32 (B) FILING DATE: 19-May-2000

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 08/836,081

37 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Bartfeld, Neil S
41 (B) REGISTRATION NUMBER: 39,901
42 (C) REFERENCE/DOCKET NUMBER: NIH099.001APC

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 619-235-8550
46 (B) TELEFAX: 619-235-0176
47 (C) TELEX:

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 26 base pairs
54 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: cDNA

59 (ix) FEATURE:

66 (A) NAME/KEY: Other
62 (B) LOCATION: 3...21
63 (D) OTHER INFORMATION: inosine

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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73 GGNTGGMANG AYTGGATHRT NGCNCC
75 (2) INFORMATION FOR SEQ ID NO: 2:
77     (i) SEQUENCE CHARACTERISTICS:
78         (A) LENGTH: 9 amino acids
79         (B) TYPE: amino acid
80         (C) STRANDEDNESS: single
81         (D) TOPOLOGY: linear
83     (ii) MOLECULE TYPE: peptide
84     (ix) FEATURE:
91         (A) NAME/KEY: Other
87         (B) LOCATION: 3...3
88         (D) OTHER INFORMATION: Xaa = Q or N
96     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
W--> 98 Gly Trp Xaa Asp Trp Ile Xaa Ala Pro
99     1           5
101 (2) INFORMATION FOR SEQ ID NO: 3:
103     (i) SEQUENCE CHARACTERISTICS:
104         (A) LENGTH: 26 base pairs
105         (B) TYPE: nucleic acid
106         (C) STRANDEDNESS: single
107         (D) TOPOLOGY: linear
109     (ii) MOLECULE TYPE: cDNA
110     (ix) FEATURE:
112         (A) NAME/KEY: Other
113         (B) LOCATION: 3...24
114         (D) OTHER INFORMATION: inosine
117     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
119 GGNTGGWSNG ARTGGATHAT NWGNCC
121 (2) INFORMATION FOR SEQ ID NO: 4:
123     (i) SEQUENCE CHARACTERISTICS:
124         (A) LENGTH: 9 amino acids
125         (B) TYPE: amino acid
126         (C) STRANDEDNESS: single
127         (D) TOPOLOGY: linear
129     (ii) MOLECULE TYPE: peptide
131     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
133 Gly Trp Ser Glu Trp Ile Ile Ser Pro
134     1           5
136 (2) INFORMATION FOR SEQ ID NO: 5:
138     (i) SEQUENCE CHARACTERISTICS:
139         (A) LENGTH: 23 base pairs
140         (B) TYPE: nucleic acid
141         (C) STRANDEDNESS: single
142         (D) TOPOLOGY: linear
144     (ii) MOLECULE TYPE: cDNA
145     (ix) FEATURE:
147         (A) NAME/KEY: Other
148         (B) LOCATION: 9...9
149         (D) OTHER INFORMATION: A or T or G or C

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152      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
154      ARRGTGTGNA CRATRGCRTG RTT
156      (2) INFORMATION FOR SEQ ID NO: 6:
158          (i) SEQUENCE CHARACTERISTICS:
159              (A) LENGTH: 8 amino acids
160              (B) TYPE: amino acid
161              (C) STRANDEDNESS: single
162              (D) TOPOLOGY: linear
164          (ii) MOLECULE TYPE: peptide
166          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
168      Asn His Ala Ile Val Gln Thr Leu
169      1          5
171      (2) INFORMATION FOR SEQ ID NO: 7:
173          (i) SEQUENCE CHARACTERISTICS:
174              (A) LENGTH: 23 base pairs
175              (B) TYPE: nucleic acid
176              (C) STRANDEDNESS: single
177              (D) TOPOLOGY: linear
179          (ii) MOLECULE TYPE: cDNA
180          (ix) FEATURE:
182              (A) NAME/KEY: Other
183              (B) LOCATION: 3...18
184              (D) OTHER INFORMATION: inosine
187          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
189      CANSCRCANS HNYBNACNAY CAT
191      (2) INFORMATION FOR SEQ ID NO: 8:
193          (i) SEQUENCE CHARACTERISTICS:
194              (A) LENGTH: 8 amino acids
195              (B) TYPE: amino acid
196              (C) STRANDEDNESS: single
197              (D) TOPOLOGY: linear
199          (ii) MOLECULE TYPE: peptide
200          (ix) FEATURE:
207              (A) NAME/KEY: Other
203              (B) LOCATION: 2...2
204              (D) OTHER INFORMATION: Xaa = V or I
219          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
W--> 221      Met Xaa Val Xaa Xaa Cys Xaa Cys
222      1          5
224      (2) INFORMATION FOR SEQ ID NO: 9:
226          (i) SEQUENCE CHARACTERISTICS:
227              (A) LENGTH: 4 amino acids
228              (B) TYPE: amino acid
229              (C) STRANDEDNESS: single
230              (D) TOPOLOGY: linear
232          (ii) MOLECULE TYPE: peptide
233          (ix) FEATURE:
240              (A) NAME/KEY: Other
236              (B) LOCATION: 2...2

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237 (D) OTHER INFORMATION: Xaa = any aa
 250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 W--> 252 Arg Xaa Xaa Xaa
 253 1
 255 (2) INFORMATION FOR SEQ ID NO: 10:
 257 (i) SEQUENCE CHARACTERISTICS:
 258 (A) LENGTH: 13 amino acids
 259 (B) TYPE: amino acid
 260 (C) STRANDEDNESS: single
 261 (D) TOPOLOGY: linear
 263 (ii) MOLECULE TYPE: peptide
 265 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 267 Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys
 268 1 5 10
 270 (2) INFORMATION FOR SEQ ID NO: 11:
 272 (i) SEQUENCE CHARACTERISTICS:
 273 (A) LENGTH: 2341 base pairs
 274 (B) TYPE: nucleic acid
 275 (C) STRANDEDNESS: single
 276 (D) TOPOLOGY: linear
 278 (ii) MOLECULE TYPE: cDNA
 280 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 282 TCAAGAACGA GTTATTTTCA GCTGCTGACT GGAGACGGTG CACGTCTGGA TACGAGAGCA 60
 283 TTTCCACTAT GGGACTGGAT ACAAACACAC ACCCGGCAGA CTTCAAGAGT TTCAGACTGA 120
 284 GGAGAAAACC TTTCCCTTCT GCTGCTACTG CTGCTGCCGC TGCTTTTGAA AGTCCACTTC 180
 285 CTTTCATGGT TTTTCCTGCC AAACCAGAGG CACCTTCGCT GCTGCCGCTG TTCTCTTTGG 240
 286 TGTCATTAGC CGGCTGGCCA GAGGATGAGA CTCCCCAAAC TCCTCACTTT CTTGCTTTGG 300
 287 TACCTGGCTT GGCTGGACCT GGAATTCATC TGCCTGTGT TGGGTGCCCC TGACTTGGGC 360
 288 CAGAGACCCC AGGGGTCCAG GCCAGGATTG GCCAAAGCAG AGGCCAAGGA GAGGCCCCCC 420
 289 CTGGCCCGGA ACGTCTTCAG GCCAGGGGGT CACAGCTATG GTGGGGGGGC CACCAATGCC 480
 290 AATGCCAGGG CAAAGGGAGG CACCGGGCAG ACAGGAGGCC TGACACAGCC CAAGAAGGAT 540
 291 GAACCCAAAA AGCTGCCCCC CAGACCGGGC GGCCCTGAAC CCAAGCCAGG ACACCCTCCC 600
 292 CAAACAAGGC AGGCTACAGC CCGGACTGTG ACCCAAAAAG GACAGCTTCC CGGAGGCAAG 660
 293 GCACCCCAAA AAGCAGGATC TGTCCCCAGC TCCTTCCTGC TGAAGAAGGC CAGGGAGCCC 720
 294 GGGCCCCCAC GAGAGCCCAA GGAGCCGTTT CGCCACCCC CCATCACACC CCACGAGTAC 780
 295 ATGCTCTCGC TGTACAGGAC GCTGTCCGAT GCTGACAGAA AGGGAGGCAA CAGCAGCGTG 840
 296 AAGTTGGAGG CTGGCCTGGC CAACACCATC ACCAGCTTTA TTGACAAAGG GCAAGATGAC 900
 297 CGAGGTCCCG TGGTCAGGAA GCAGAGGTAC GTGTTTGACA TTAGTGCCCT GGAGAAGGAT 960
 298 GGGCTGCTGG GGGCCGAGCT GCGGATCTTG CGGAAGAAGC CCTCGGACAC GGCCAAGCCA 1020
 299 GCGGTCCCCC GGAGCCGGCG GGCTGCCAG CTGAAGCTGT CCAGCTGCCC CAGCGGCCCG 1080
 300 CAGCCGGCCG CCTTGCTGGA TGTGCGCTCC GTGCCAGGCC TGGACGGATC TGGCTGGGAG 1140
 301 GTGTTTCGACA TCTGGAAGCT CTTCCGAAAC TTAAAGAACT CGGCCAGCT GTGCCTGGAG 1200
 302 CTGGAGGCCT GGAACGGGG CAGGACCGTG GACCTCCGTG GCCTGGGCTT CGACCGCGCC 1260
 303 GCCCGGCAGG TCCACGAGAA GGCCCTGTTC CTGGTGTTG GCCGCACCAA GAAACGGGAC 1320
 304 CTGTTCTTTA ATGAGATTAA GGCCGCTCT GGCCAGGACG ATAAGACCGT GTATGAGTAC 1380
 305 CTGTTTCAGC AGCGGCGAAA ACGGCGGGCC CCATCGGCCA CTCGCCAGGG CAAGCGACCC 1440
 306 AGCAAGAACC TTAAGGCTCG CTGCAGTCGG AAGGCACTGC ATGTCAACTT CAAGGACATG 1500
 307 GGCTGGGACG ACTGGATCAT CGCACCCCTT GAGTACGAGG CTTTCCACTG CGAGGGGCTG 1560
 308 TGCGAGTTCC CATTGCGCTC CCACCTGGAG CCCACGAATC ATGCAGTCAT CCAGACCCTG 1620

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309 ATGAACTCGA TGGACCCCGA GTCCACACCA CCCACCTGCT GTGTGCCCAC GCGGCTGAGT 1680
310 CCCATCAGCA TCCTCTTCAT TGAATCTGCC AACAACTGGG TGTATAAGCA GTATGAGGAC 1740
311 ATGGTCGTGG AGTCGTGTGG CTGCAGGTAG CAGCACTGGC CCTCTGTCTT CCTGGGTGGC 1800
312 ACATCCCAAG AGCCCCCTTC TGAATCTCTG GAATCACAGA GGGGTCAGGA AGCTGTGGCA 1860
313 GGAGCATCTA CACAGCTTGG TGAAGGGATT CAATAAGCTT GCTCGCTCTC TGAGTGTGAC 1920
314 TTGGGCTAAA GGCCCCCTTT TATCCACAAG TTCCCCTGGC TGAGGATTGC TGCCCGTCTG 1980
315 CTGATGTGAC CAGTGGCAGG CACAGGTCCA GGGAGACAGA CTCTGAATGG GACTGAGTCC 2040
316 CAGGAAACAG TGCTTTCCGA TGAGACTCAG CCCACCATTT CTCCTCACCT GGGCCTTCTC 2100
317 AGCCTCTGGA CTCTCCTAAG CACCTCTCAG GAGAGCCACA GGTGCCACTG CCTCCTCAAA 2160
318 TCACATTTGT GCCTGGTGAC TTCCTGTCCC TGGGACAGTT GAGAAGCTGA CTGGGCAAGA 2220
319 GTGGGAGAGA AGAGGAGAGG GCTTGGATAG AGTTGAGGAG TGTGAGGCTG TTAGACTGTT 2280
320 AGATTTAAAT GTATATTGAT GAGATAAAAA GCAAAACTGT GCCTAAAAAA AAAAAAAAAA 2340
321 A 2341
323 (2) INFORMATION FOR SEQ ID NO: 12:
325 (i) SEQUENCE CHARACTERISTICS:
326 (A) LENGTH: 1308 base pairs
327 (B) TYPE: nucleic acid
328 (C) STRANDEDNESS: single
329 (D) TOPOLOGY: linear
331 (ii) MOLECULE TYPE: cDNA
333 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
335 CGAGCGTCCG CCGAGCTGGG CTCCGCCAAG GGAATGCGAA CGCGCAAGGA AGGAAGGATG 60
336 CCGCGGGCGC CGAGAGAGAA TGCCACGGCC CGGGAGCCCC TGGATCGCCA GGAGCCCCCG 120
337 CCGAGGCCGC AGGAGGAGCC CCAGCGGCGG CCGCCACAGC AGCCTGAAGC TCGGGAGCCT 180
338 CCCGGCAGGG GCCCCGCGTT GGTGCCCCAC GAGTACATGC TGTCAATCTA CAGGACTTAC 240
339 TCCATCGCCG AGAAGCTGGG CATCAATGCT AGCTTTTTC AGTCTTCAA GTCGGCTAAT 300
340 ACGATCACTA GCTTTGTAGA CAGGGGACTA GACGATCTCT CGCACACTCC TCTCCGGAGA 360
341 CAGAAGTATT TGTTTGATGT GTCCACGCTC TCAGACAAAG AAGAGCTGGT GGGCGCGGAC 420
342 GTGCGGCTGT TTCGCCAGGC GCCCGCTGCC CTGGCGCCGC CGGCGGCCGC TCCGCTTGCA 480
343 GCTCTTCGCC TGCCAGTCGC CCCTGCTGCT GGAAGCGCGG AGCCTGGACC CGCAGGGGCG 540
344 CCCCAGCCCC GCTGGGAAGT CTTGACGCTG TGGCGGGGCC TGCGCCCCCA GCCCTGGAAG 600
345 CAGCTGTGCT TGGAGCTTCG GGCCGCGTGG GGCGGCGAGC CGGGCGCCGC GGAGGACGAG 660
346 GCGCGCACGC CTGGGCCCCA GCAGCCGCCG CCCCCGGACC TGCGGAGTCT GGGCTTCGGC 720
347 CGGAGGGTGC GGACCCCCCA GGAGCGCGCC TTGCTCGTCG TGTTCTCCAG GTCCAGCGC 780
348 AAGACCTGT TCGCCGAGAT GCGCGAGCAG CTGGGCTCGG CGACCGAGGT GGTGCGCCCC 840
349 GGTGGTGGGG CCGAGGGGTC GGGGCCGCCG CCGCCGCCGC CGCCGCCGCC GCCGTCGGG 900
350 ACCCCGACG CTGGGCTCTG GTCGCCCTCG CCTGGCCGCG GCGGCGCAC GGCCTTCGCC 960
351 AGCCGCCACG GCAAGCGGCA CGCAAGAAG TCGAGGCTGC GCTGCAGCAA GAAGCCCCCTG 1020
352 CACGTGAACT TCAAGGAGCT GGGCTGGGAC GACTGGATTA TCGCGCCCCC GGAGTACGAG 1080
353 GCCTACCACT GCGAGGGCGT GTGCGACTTC CCGCTACGCT CGCACCTGGA GCCACCAAC 1140
354 CACGCCATCA TCCAGACGCT GATGAACTCC ATGGACCCCC GCTCCACCCC GCCAGCTGC 1200
355 TGCGTGCCCA CCAAATTGAC TCCCATCAGC ATCTTGATCA TCGACGCGGG CAATAATGTG 1260
356 GTCTACAACG AGTACGAGGA GATGGTGGTG GAGTCGTGCG GCTGCAGG 1308
358 (2) INFORMATION FOR SEQ ID NO: 13:
360 (i) SEQUENCE CHARACTERISTICS:
361 (A) LENGTH: 501 amino acids
362 (B) TYPE: amino acid
363 (C) STRANDEDNESS: single
364 (D) TOPOLOGY: linear

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VERIFICATION SUMMARY

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15